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#13
8-2802
P.2

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/856,320A

DATE: 08/21/2002

TIME: 13:25:29

Input Set : A:\sequence listing.txt

Output Set: N:\CRF3\08202002\I856320A.raw

ENTERED

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3 <110> APPLICANT: UEMURA, Hidetoshi
4     OKUI, Akira
5     KOMINAMI, Katsuya
6     YAMAGUCHI, Nozomi
7     MITSUI, Shinichi
9 <120> TITLE OF INVENTION: NOVEL SERINE PROTEASE BSSP6
11 <130> FILE REFERENCE: UEMURA=4
13 <140> CURRENT APPLICATION NUMBER: 09/856,320A
14 <141> CURRENT FILING DATE: 2001-05-21
16 <150> PRIOR APPLICATION NUMBER: JP 10-347802
17 <151> PRIOR FILING DATE: 1998-11-20
19 <160> NUMBER OF SEQ ID NOS: 41
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1301
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (113)..(958)
31 <223> OTHER INFORMATION:
33 <220> FEATURE:
34 <221> NAME/KEY: mat_peptide
35 <222> LOCATION: (272)..()
36 <223> OTHER INFORMATION:
38 <400> SEQUENCE: 1
39 ctgccttgct ccacacctgg tcaggggaga gaggggagga aagccaaggg aagggaccta      60
41 actgaaaaca aacaagctgg gagaagcagg aatctgcgct cgggttcgcg ag atg cag      118
42                                     Met Gln
45 agg ttg agg tgg ctg cgg gac tgg aag tca tcg ggc aga ggt ctc aca      166
46 Arg Leu Arg Trp Leu Arg Asp Trp Lys Ser Ser Gly Arg Gly Leu Thr
47 -50 -45 -40
49 gca gcc aag gaa cct ggg gcc cgc tcc tcc ccc ctc cag gcc atg agg      214
50 Ala Ala Lys Glu Pro Gly Ala Arg Ser Ser Pro Leu Gln Ala Met Arg
51 -35 -30 -25 -20
53 att ctg cag tta atc ctg ctt gct ctg gca aca ggg ctt gta ggg gga      262
54 Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val Gly Gly
55 -15 -10 -5
57 gag acc agg atc atc aag ggg ttc gag tgc aag cct cac tcc cag ccc      310
58 Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser Gln Pro
59 -1 1 5 10
61 tgg cag gca gcc ctg ttc gag aag acg cgg cta ctc tgt ggg gcg acg      358
62 Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala Thr

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63      15      20      25
65 ctc atc gcc ccc aga tgg ctc ctg aca gca gcc cac tgc ctc aag ccc      406
66 Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys Pro
67 30      35      40      45
69 cgc tac ata gtt cac ctg ggg cag cac aac ctc cag aag gag gag ggc      454
70 Arg Tyr Ile Val His Leu Gly Gln His Asn Leu Gln Lys Glu Glu Gly
71      50      55      60
73 tgt gag cag acc cgg aca gcc act gag tcc ttc ccc cac ccc ggc ttc      502
74 Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro Gly Phe
75      65      70      75
77 aac aac agc ctc ccc aac aaa gac cac cgc aat gac atc atg ctg gtg      550
78 Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met Leu Val
79      80      85      90
81 aag atg gca tcg cca gtc tcc atc acc tgg gct gtg cga ccc ctc acc      598
82 Lys Met Ala Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro Leu Thr
83      95      100      105
85 ctc tcc tca cgc tgt gtc act gct ggc acc agc tgc ctc att tcc ggc      646
86 Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly
87 110      115      120      125
89 tgg ggc agc acg tcc agc ccc cag tta cgc ctg cct cac acc ttg cga      694
90 Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg
91      130      135      140
93 tgc gcc aac atc acc atc att gag cac cag aag tgt gag aac gcc tac      742
94 Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr
95      145      150      155
97 ccc ggc aac atc aca gac acc atg gtg tgt gcc agc gtg cag gaa ggg      790
98 Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly
99      160      165      170
101 ggc aag gac tcc tgc cag ggt gac tcc ggg ggc cct ctg gtc tgt aac      838
102 Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn
103      175      180      185
105 cag tct ctt caa ggc att atc tcc tgg ggc cag gat ccg tgt gcg atc      886
106 Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala Ile
107 190      195      200      205
109 acc cga aag cct ggt gtc tac acg aaa gtc tgc aaa tat gtg gac tgg      934
110 Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val Asp Trp
111      210      215      220
113 atc cag gag acg atg aag aac aat tagactggac ccacccacca cagcccatca      988
114 Ile Gln Glu Thr Met Lys Asn Asn
115      225
117 cccctccatctt ccacttggtg tttggttcct gttcactctg ttaataagaa accctaagcc      1048
119 aagaccctct acgaacattc tttgggcctc ctggactaca ggagatgctg tcacttaata      1108
121 atcaacctgg ggttcgaaat cagtgaagacc tggattcaaa ttctgccttg aaatattgtg      1168
123 actctgggaa tgacaacacc tggtttgttc tctgttgtat cccagcccc aaagacagct      1228
125 cctggccata tatcaaggtt tcaataaata tttgctaaat gaaaaaaaa aaaaaaaaa      1288
127 aaaaaaaaaaaa aaa      1301
130 <210> SEQ ID NO: 2
131 <211> LENGTH: 282
132 <212> TYPE: PRT

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133 <213> ORGANISM: Homo sapiens
135 <400> SEQUENCE: 2
137 Met Gln Arg Leu Arg Trp Leu Arg Asp Trp Lys Ser Ser Gly Arg Gly
138           -50           -45           -40
141 Leu Thr Ala Ala Lys Glu Pro Gly Ala Arg Ser Ser Pro Leu Gln Ala
142           -35           -30           -25
145 Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val
146           -20           -15           -10
149 Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser
150 -5           -1 1           5           10
153 Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly
154           15           20           25
157 Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu
158           30           35           40
161 Lys Pro Arg Tyr Ile Val His Leu Gly Gln His Asn Leu Gln Lys Glu
162           45           50           55
165 Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro
166 60           65           70           75
169 Gly Phe Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met
170           80           85           90
173 Leu Val Lys Met Ala Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro
174           95           100           105
177 Leu Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile
178           110           115           120
181 Ser Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr
182           125           130           135
185 Leu Arg Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn
186 140           145           150           155
189 Ala Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln
190           160           165           170
193 Glu Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
194           175           180           185
197 Cys Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys
198           190           195           200
201 Ala Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val
202           205           210           215
205 Asp Trp Ile Gln Glu Thr Met Lys Asn Asn
206 220           225
209 <210> SEQ ID NO: 3
210 <211> LENGTH: 1323
211 <212> TYPE: DNA
212 <213> ORGANISM: Mus sp.
214 <220> FEATURE:
215 <221> NAME/KEY: CDS
216 <222> LOCATION: (103)..(930)
217 <223> OTHER INFORMATION:
219 <220> FEATURE:
220 <221> NAME/KEY: mat_peptide
221 <222> LOCATION: (244)..()

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Input Set : A:\sequence listing.txt

Output Set: N:\CRF3\08202002\I856320A.raw

222 <223> OTHER INFORMATION:

224 <400> SEQUENCE: 3

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225 ccacatctga ctagggaagt aaggcgaagg aggcccatgg aagaaaaatc taaatgaaaa      60
227 cataagctag gagaactgag gcttcaaacc tgaagctatc ta atg agg agg ctg      114
228                               Met Arg Arg Leu
229                               -45
231 aag agt gac tgg aaa tta tct aca gaa acc agg gaa cct ggc gcc cgc      162
232 Lys Ser Asp Trp Lys Leu Ser Thr Glu Thr Arg Glu Pro Gly Ala Arg
233           -40                               -35           -30
235 cct gcc cta ctc cag gcc agg atg att ctc cga ctc att gca ctt gct      210
236 Pro Ala Leu Leu Gln Ala Arg Met Ile Leu Arg Leu Ile Ala Leu Ala
237           -25                               -20           -15
239 ctg gta aca ggg cac gta ggg gga gag acg agg atc atc aag ggt tat      258
240 Leu Val Thr Gly His Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Tyr
241           -10                               -5           -1 1           5
243 gag tgc agg cct cac tca cag cca tgg cag gtg gcc ctc ttt cag aag      306
244 Glu Cys Arg Pro His Ser Gln Pro Trp Gln Val Ala Leu Phe Gln Lys
245           10                               15           20
247 aca cgg ctt ctc tgt ggg gca acc ctc atc gcc ccc aaa tgg ctc ctg      354
248 Thr Arg Leu Leu Cys Gly Ala Thr Leu Ile Ala Pro Lys Trp Leu Leu
249           25                               30           35
251 aca gca gcc cac tgc cgc aag ccc cat tac gtg atc ctc ctt gga gag      402
252 Thr Ala Ala His Cys Arg Lys Pro His Tyr Val Ile Leu Leu Gly Glu
253           40                               45           50
255 cac aat cta gag aag aca gac ggc tgt gag cag agg cgg atg gcc act      450
256 His Asn Leu Glu Lys Thr Asp Gly Cys Glu Gln Arg Arg Met Ala Thr
257           55                               60           65
259 gag tcc ttc ccc cac ccc gac ttc aac aac agc ctc ccc aac aaa gac      498
260 Glu Ser Phe Pro His Pro Asp Phe Asn Asn Ser Leu Pro Asn Lys Asp
261 70           75           80           85
263 cac cgg aat gac ata atg ctt gtg aag atg tgc tct ccc gtc ttc ttt      546
264 His Arg Asn Asp Ile Met Leu Val Lys Met Ser Ser Pro Val Phe Phe
265           90           95           100
267 acc cga gct gtg cag cca ctc acc ctg tcc cca cac tgt gtc gct gca      594
268 Thr Arg Ala Val Gln Pro Leu Thr Leu Ser Pro His Cys Val Ala Ala
269           105           110           115
271 ggc acc agc tgc ctc att tct gga tgg ggc acc acg tcc agc ccc cag      642
272 Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Thr Thr Ser Ser Pro Gln
273           120           125           130
275 ttg cgc ctg cct cat tcc ttg cga tgt gcc aat gtc tcc atc atc gaa      690
276 Leu Arg Leu Pro His Ser Leu Arg Cys Ala Asn Val Ser Ile Ile Glu
277           135           140           145
279 cac aag gag tgt gag aag gcc tac ccg ggc aac atc aca gac acc atg      738
280 His Lys Glu Cys Glu Lys Ala Tyr Pro Gly Asn Ile Thr Asp Thr Met
281 150           155           160           165
283 ctg tgc gcc agt gtt cgg aaa gag ggc aag gac tcc tgt cag ggt gac      786
284 Leu Cys Ala Ser Val Arg Lys Glu Gly Lys Asp Ser Cys Gln Gly Asp
285           170           175           180
287 tct gga ggc ccc ctg gtc tgc aac gga tct ctt caa ggc atc atc tcc      834

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288 Ser Gly Gly Pro Leu Val Cys Asn Gly Ser Leu Gln Gly Ile Ile Ser
289          185          190          195
291 tgg ggt cag gac cca tgt gcc gtc acc aga aag cct ggt gtc tat aca      882
292 Trp Gly Gln Asp Pro Cys Ala Val Thr Arg Lys Pro Gly Val Tyr Thr
293          200          205          210
295 aaa gtc tgc aaa tac ttt aac tgg atc cac gag gtt atg agg aac aat      930
296 Lys Val Cys Lys Tyr Phe Asn Trp Ile His Glu Val Met Arg Asn Asn
297          215          220          225
299 tagaggggac ctgcttccca ccacccaacc cctccaacct cttcttaatg ctttgacttc      990
301 tottcattct gccctaagaa gtcctcagct gggaccctgg catgtactct ctccgaccca      1050
303 ccatgagtat agtatagga tgctctaact tgatgatcga cctggggcct ggaatcaaat      1110
305 cctgacttga actaaattgt gactctggac atgataacca ctggttttgt ttgtttggtt      1170
307 gttttttgtt ttgttttgtt ttgttcccag ctttgaagac agtcctggc atatcccagg      1230
309 gtttcaataa atatttgta aatgataaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1290
311 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa                                1323
314 <210> SEQ ID NO: 4
315 <211> LENGTH: 276
316 <212> TYPE: PRT
317 <213> ORGANISM: Mus sp.
319 <400> SEQUENCE: 4
321 Met Arg Arg Leu Lys Ser Asp Trp Lys Leu Ser Thr Glu Thr Arg Glu
322          -45          -40          -35
325 Pro Gly Ala Arg Pro Ala Leu Leu Gln Ala Arg Met Ile Leu Arg Leu
326          -30          -25          -20
329 Ile Ala Leu Ala Leu Val Thr Gly His Val Gly Gly Glu Thr Arg Ile
330          -15          -10          -5          -1 1
333 Ile Lys Gly Tyr Glu Cys Arg Pro His Ser Gln Pro Trp Gln Val Ala
334          5          10          15
337 Leu Phe Gln Lys Thr Arg Leu Leu Cys Gly Ala Thr Leu Ile Ala Pro
338          20          25          30
341 Lys Trp Leu Leu Thr Ala Ala His Cys Arg Lys Pro His Tyr Val Ile
342          35          40          45
345 Leu Leu Gly Glu His Asn Leu Glu Lys Thr Asp Gly Cys Glu Gln Arg
346          50          55          60          65
349 Arg Met Ala Thr Glu Ser Phe Pro His Pro Asp Phe Asn Asn Ser Leu
350          70          75          80
353 Pro Asn Lys Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ser Ser
354          85          90          95
357 Pro Val Phe Thr Arg Ala Val Gln Pro Leu Thr Leu Ser Pro His
358          100          105          110
361 Cys Val Ala Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Thr Thr
362          115          120          125
365 Ser Ser Pro Gln Leu Arg Leu Pro His Ser Leu Arg Cys Ala Asn Val
366          130          135          140          145
369 Ser Ile Ile Glu His Lys Glu Cys Glu Lys Ala Tyr Pro Gly Asn Ile
370          150          155          160
373 Thr Asp Thr Met Leu Cys Ala Ser Val Arg Lys Glu Gly Lys Asp Ser
374          165          170          175
377 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gly Ser Leu Gln

```

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\sequence listing.txt

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L:969 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36

L:994 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37